

<u>File Name</u>	<u>Date Created</u>	<u>Size (bytes)</u>
MakeHelp.bat	09/27/2000	1,594
newlibrarynamedlg.cpp	10/05/2000	1,926
newlibrarynamedlg.h	09/29/2000	883
resource.h	02/06/2001	8,530
resource.hm	02/06/2001	4,528
startdlg.cpp	10/23/2000	3,742
startdlg.h	10/23/2000	1,093
StdAfx.cpp	10/11/2000	221
StdAfx.h	10/03/2000	602
SubtractionLibraryUtility.cpp	10/11/2000	4,047
SubtractionLibraryUtility.h	02/06/2001	6,385
SubtractionLibraryUtility.hpj	02/06/2001	2,624
SubtractionLibraryUtility.rc	07/25/2001	28,316
SubtractionLibraryUtilityDlg.cpp	06/21/2001	209,771
SubtractionLibraryUtilityDlg.h	04/16/2001	6,943
SubtractionLibraryUtility.hm	08/09/2001	663
TimedMessage.cpp	10/27/2000	1,718
TimedMessage.h	10/27/2000	875
trimdialog.cpp	11/06/2000	119,594
trimdialog.h	11/06/2000	4,099
TUTORIAL PRIMERS.VEC	06/08/2001	2,039
TUTORIAL001.Seq	06/11/2001	640

Replace the paragraph at page 8, line 3, with the following paragraph:

--BRIEF DESCRIPTION OF THE DRAWING

*A2*  
Fig. 1 shows a file directory structure for one embodiment of the invention.

Fig. 2 shows a Main User Interface computer display.

Fig. 3 (SEQ ID NOS 7, 9 and 12-16) shows a Trimming Interface computer display.--

Replace Table 2. beginning on page 18 with the following rewritten Table 2.

--Table 2.

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Schlager's BLAST UTILITY, RESECO @1999  
 Results from file \\r5840\pub\MolTox\blast\TRIMMED\MB2D\M2r02\_NV.SEQ  
 BLAST search done 4/5/2000

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HTTP/1.0 200 OK MIME-Version: 1.0 Content-type: text/html

The query sequence for this search has been filtered. Filtering eliminates low complexity regions that commonly give spuriously high scores that reflect compositional bias rather than significant position-by-position alignment. Filtering can eliminate these potentially confounding matches (e.g., hits against proline-rich regions or poly-A tails) from the blast reports, leaving regions whose blast statistics reflect the specificity of their pairwise alignment.

BLASTN 2.0.11 [Jan-20-2000]

Reference: Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Query= RESECO BLAST

UTILITY: \\r5840\pub\MolTox\blast\TRIMMED\MB2D\M2r02\_NV.SEQ  
 (561 letters)

Database: nt

607,850 sequences; 1,816,255,750 total letters

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	Score	E
Sequences producing significant alignments:		
gi 3228368 gb K02061.1 MUSRPL4A Mus musculus L32-4A pseudog...	565	<b>e-159</b>
gi 6981481 ref NM_013226.1   Rattus norvegicus ribosomal pr...	452	<b>e-125</b>

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gi|3228368|gb|K02061.1|MUSRPL4A Mus musculus L32-4A pseudogene, complete seq  
 Length = 1516

Score = 565 bits (285), Expect = e-159  
 Identities = 360/384 (93%), Gaps = 5/384 (1%)  
 Strand = Plus / Minus

Query: SEQ ID NO: 1

```
38 gcaagggtttgtgatTTTatTTaaacataaaacatgcacacaagccatctactcatttct 97
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Sbjct: SEQ ID NO: 2

```
1094 gcaagggtttgtgatTTTatTTaaacataaaacatgcacacaagccatctattcatttct 1035
```

Query: 98 tcgtcgtagcctggcgttggatggactctgatggccagctgtgctgtctttct 157

```
||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
```

Sbjct: 1034 tcgtcgtagcctggcgttggatggactctgatggccagctgtgctgtctttct 975

Query: 158 acaatggctttcagttctanaggacacattgtgagcaatctcagcacagtaagattg 217

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||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
```

Sbjct: 974 acaatggctttcgggtttagaggacacattgtgagcaatctcagcacagtaagattg 915

Query: 218 ttgcacatcagcagcacccagctccttgacattgtggaccannaacttgcggaaancg 277

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||||||||| |||||||||||||||||||||||||||||||||||||||||||||
```

Sbjct: 914 ttgcacatcagcagcacccagctccttgacattgtggaccaggaacttgcggaaagccg 855

Query: 278 ctgggcagcatgtgcttggtttcttggcttgcacaaaccgaagttnngcatcangat 337  
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 854 ctgggcagcatgtgcttggtttcttggcttgcacaaaccgaagttnngcatcaggat 796  
 Query: 338 ntggcccttgaaccttctcc-ccnccctgttgcacaaaccgaagttnngcatcangat 394  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 795 ctggcccttgaaccttctccgcacccctgttgcacaaaccgaagttnngcatcaggat 736  
 Query: 395 cttaa-tttccatatcggtctga 417  
 ||||| ||||| ||||| |||||  
 Sbjct: 735 cttaatttcacatatcggtctga 712

gi|6981481|ref|NM\_013226.1|| Rattus norvegicus ribsml protein L32(Rpl32), mRNA

Length = 465  
 Score = 452 bits (228), Expect = e-125  
 Identities = 319/350 (91%), Gaps = 2/350 (0%)  
 Strand = Plus / Minus  
 Query: SEQ ID NO: 3  
 38 gcaggtttgtgattttatcaaataaaaacatgcacacaagccatctactcatttct 97  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: SEQ ID NO: 4  
 461 gcagttttgtggtttatgttgcacacaaaacaggcacacaagccatctattcattct 402  
 Query: 98 tcgcgtcgtaancctggcgttggatttgtactctgtatggccagctgtgtctttct 157  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 401 tcgcgtcgtaggcctggcgttggatttgtactctgtatggccagctgtgtctttct 342  
 Query: 158 acaatggctttcagttcttanaggacacattgtgagcaatctcagcacagtaagatttg 217  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 341 acgatggctttcggttcttagaggacacattgtgagcaatctcagcacagtaagatttg 282  
 Query: 218 ttgcacatcagcagcacccctcagctcattgtggaccannaacttgcgganccg 277  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 281 ttgcacatcagcagcacccctcagctcattgtggaccagaacttccggagccg 222  
 Query: 278 ctggcagcatgtgcttggtttcttggcttgcacaaaccgaagttnngcatcangat 337  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Sbjct: 221 ctaggcagcatgtgcttggtttcttactcccgttaacc-aatgttggcatcaggat 163  
 Query: 338 ntggcccttgaaccttctcc-ccnccctgttgcacaaaccgaagttnngcatcaggat 386  
 ||||| ||||| ||||| |||||  
 Sbjct: 162 ctggcccttgaatcttccgcacccctgttgcacaaaccgaagttnngcatcangat 113

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Database: nt  
 Posted date: Mar 30, 2000 10:02 PM  
 Number of letters in database: 1,816,255,750  
 Number of sequences in database: 607,850

Lambda K H  
 1.37 0.711 0.00  
 Gapped  
 Lambda K H  
 1.37 0.711 4.94e-324  
 Matrix: blastn matrix:1 -3  
 Gap Penalties: Existence: 5, Extension: 2  
 Number of Hits to DB: 420761  
 Number of Sequences: 607850  
 Number of extensions: 420761  
 Number of successful extensions: 34073  
 Number of sequences better than 10.0: 52  
 length of query: 561  
 length of database: 1,816,255,750

effective HSP length: 20  
effective length of query: 541  
effective length of database: 1,804,098,750  
effective search space: 976017423750  
effective search space used: 976017423750  
T: 0  
A: 0  
X1: 6 (11.9 bits)  
X2: 10 (19.8 bits)  
S1: 12 (24.3 bits)  
S2: 19 (38.2 bits)

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Replace the label for Table 3. at page 20, line 8, with the following label:

*N.G.* *7--Table 3. (SEQ ID NO: 5)--*  
*Where*

Replace the paragraph at page 24, line 7 with the following paragraph:

*Ack*  
-- A vector file must be customized for a particular laboratory and selected prior to the trimming step. The vectors files are formatted using a six line, ASCII text format. Only the first contiguous string of letters on each line is read, so the remainder of each line can be used for annotations. Each line starts with a nucleotide sequence. An example vector file is presented below (SEQ ID NOS 6-11, respectively in order of appearance):

AGCGGCCGCCGGGCAGGTC // positive insertion orientation 5' adapter sequence  
ACCTCggccgaccacgct // positive insertion orientation 3' adapter sequence  
TTACTAGTGGATCCGAGCTCGGTACCAAGCTTC // forward direction confirm  
fragment 25 bases after 3' adapter  
AGCGTGGTCGCGGCCGAGGT // negative insertion orientation 5' adapter sequence  
ACCTGCCGGCGGCCGCTC // negative insertion orientation 3' adapter sequence  
CACACTGGCGGCCGCTCGAGCATGCATCTAGAG // reverse direction confirm fragment  
25 bases after 3' adapter. --